

Fig.1

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MBP  
 SP-A  
 SP-D

MSLPFS-LPLLLSMVAASVSETVTCEDAQKI---CPAVIACSS--PGINGFPCKDGRDGTKEKGEFG  
 MWLCPLALTLILMA-----ASGAACEVKDVQV-----GSPG  
 MLLFLI-SALVLLITQ-PLGLYEAEMKTYSHRITPSACTLV-MCSSLVESGLPGRDGRDGRGPRGEKGDPG 70

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 IPGTFCGSHGLPGRDGR---DGVKGDPPGPMGPPG---EHP  
 LPGAAGQAQMPGOAGPVGPKGDNGSVGEPPGPKGDTGPSGPPGPPGVPGPAGRECPGKQCNIGPQKPGP 140

-----  
 QGLRGLQGP-----PGKLGPPPCNPGPSGSPGPKGCK  
 CPGCNGLPGAPGVPE-----RGEKGEPPGERGPPGL  
 KGEAGPKGEVGAPGMQGSACARGLAGPKGCGVMPGERGVPGNAGAAGSAGAMGPGGSPGANRGPGLKGDK 210

Fig.2

Fig. 3



Fig. 4

[illegible]

Fig. 5

MBP GQKGDPG-KSPDGDSSLAA-----SERKALQTEMARIKKWLTFSLGKQVCNKFFLTNGEIMTF  
SP-A PAHLDEELQATLHD---FRHQILQTRGALS-LQGSI-----MTVGEKVFSNQSITF  
SP-D GDKGIPGDKGAKGESGLPDVASLRQQVEALQGOVQHLQAAPFSQYKKVELFPNGQSVGEKITEKTAGFVKPF  
-----IVCDGGRYRKFGVGLDISIARLKISMKFVKN--VIAGIRETEEFYIVQEEKNY 280

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EKKVLCVKFQASVATPRNAAENCAIQNL I---KEE-AFLGITDEKTEGQFVDLTGNRLT-YTNWNEGEP  
DAIQEACARAGGRIAMPNPEENEAIASFVKKYNITY-AVVGITDEGSPGDFRYSDDGTPVN-YTNWYRGE  
TEAQLLCTQAGGCLASPRSAAENALQQLVAKNEA-AFLSMTDSKTEGKFTYPTGESLV-YSNWAPGEP  
RESLTHCIRIRGGMLAMPKDEANNTLIAADYAKSGOFFRVFIGVNDLEREGQYMFDTNPTLQNYSNWNEGEP 350

NNAGSDEDCVLLKNGQWNDVPCSTSHLAVCEFI\*---  
AGRG-KEQCCEMYTIDGQWDRNCLYSRLTICEF\*---  
NDDGSEDCVEIFITNGKWNDRACGEKRLVVCEF\*---  
SDPYGHEDCCEVMLSSGRWNDTECHLTMYFVCEFIKKKK\*

Fig. 6

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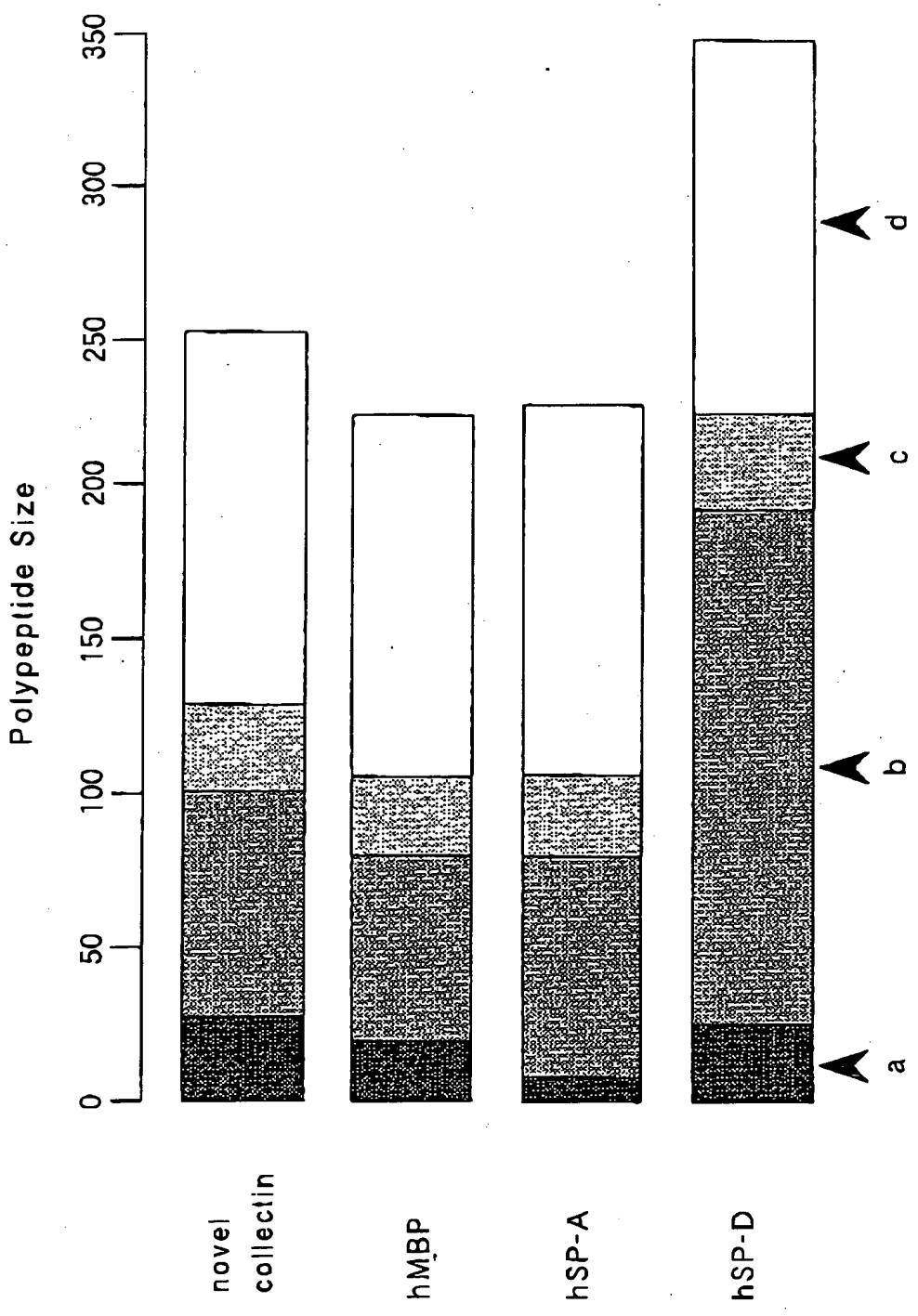


Fig.7

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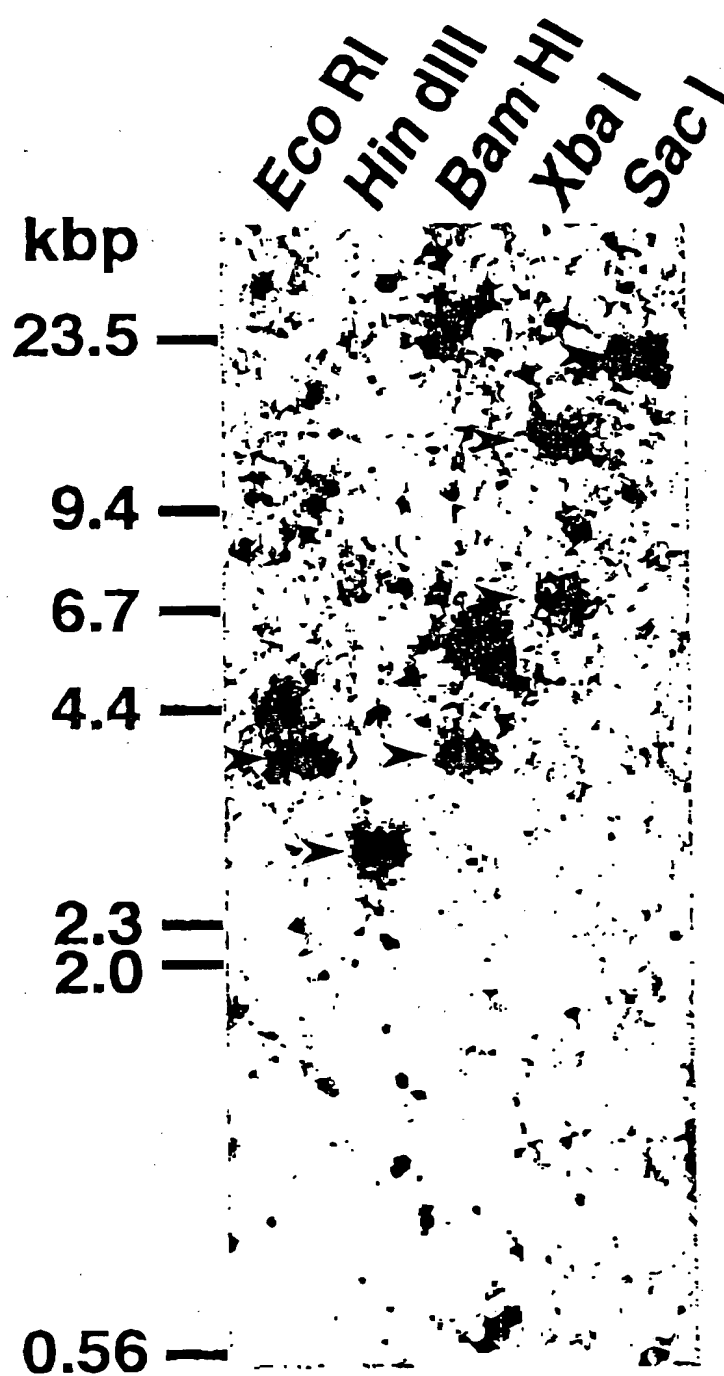


Fig. 8



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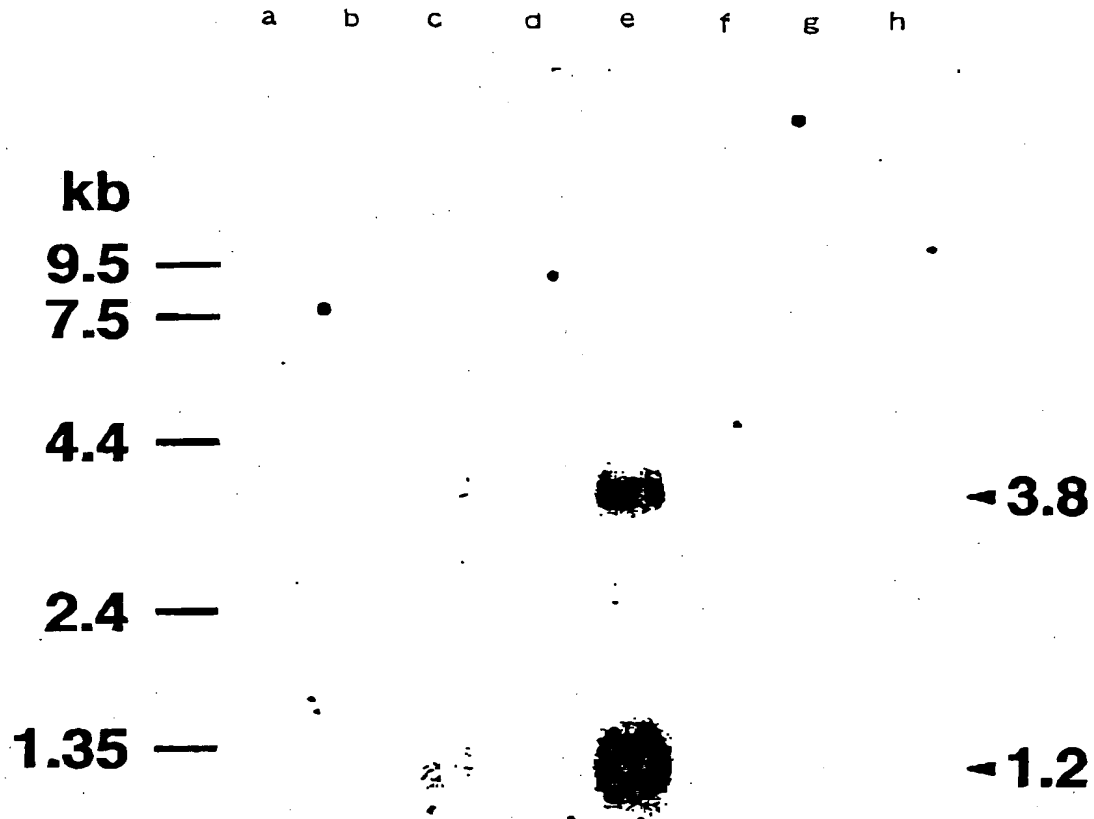


Fig. 9

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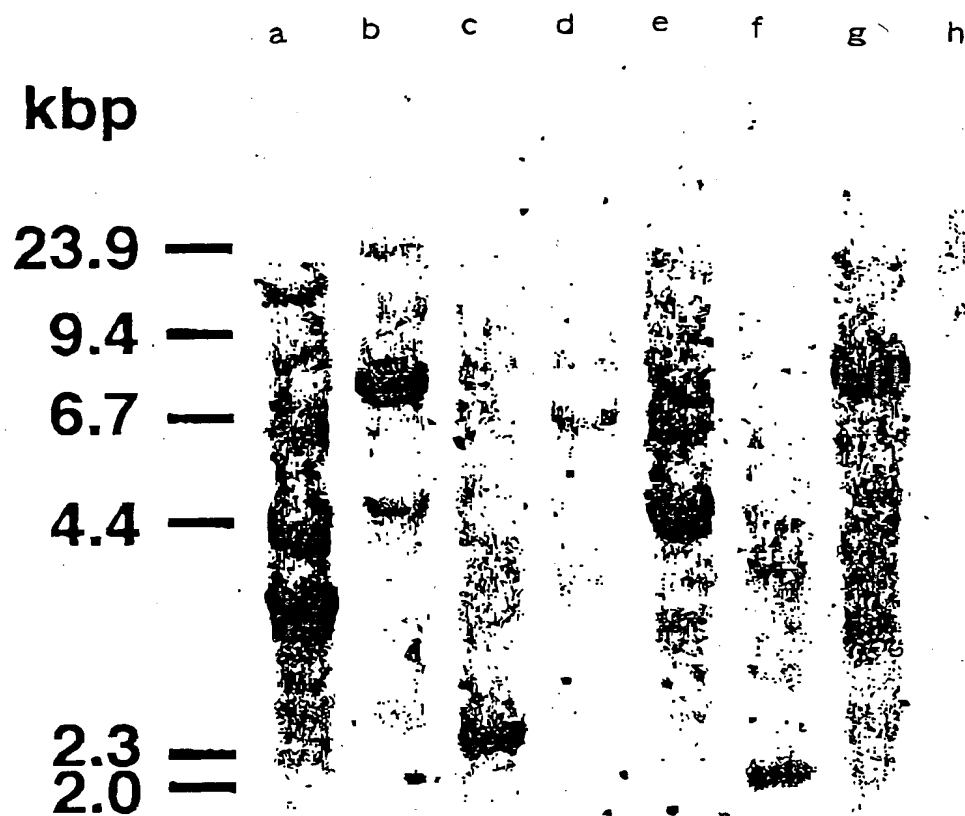


Fig.10

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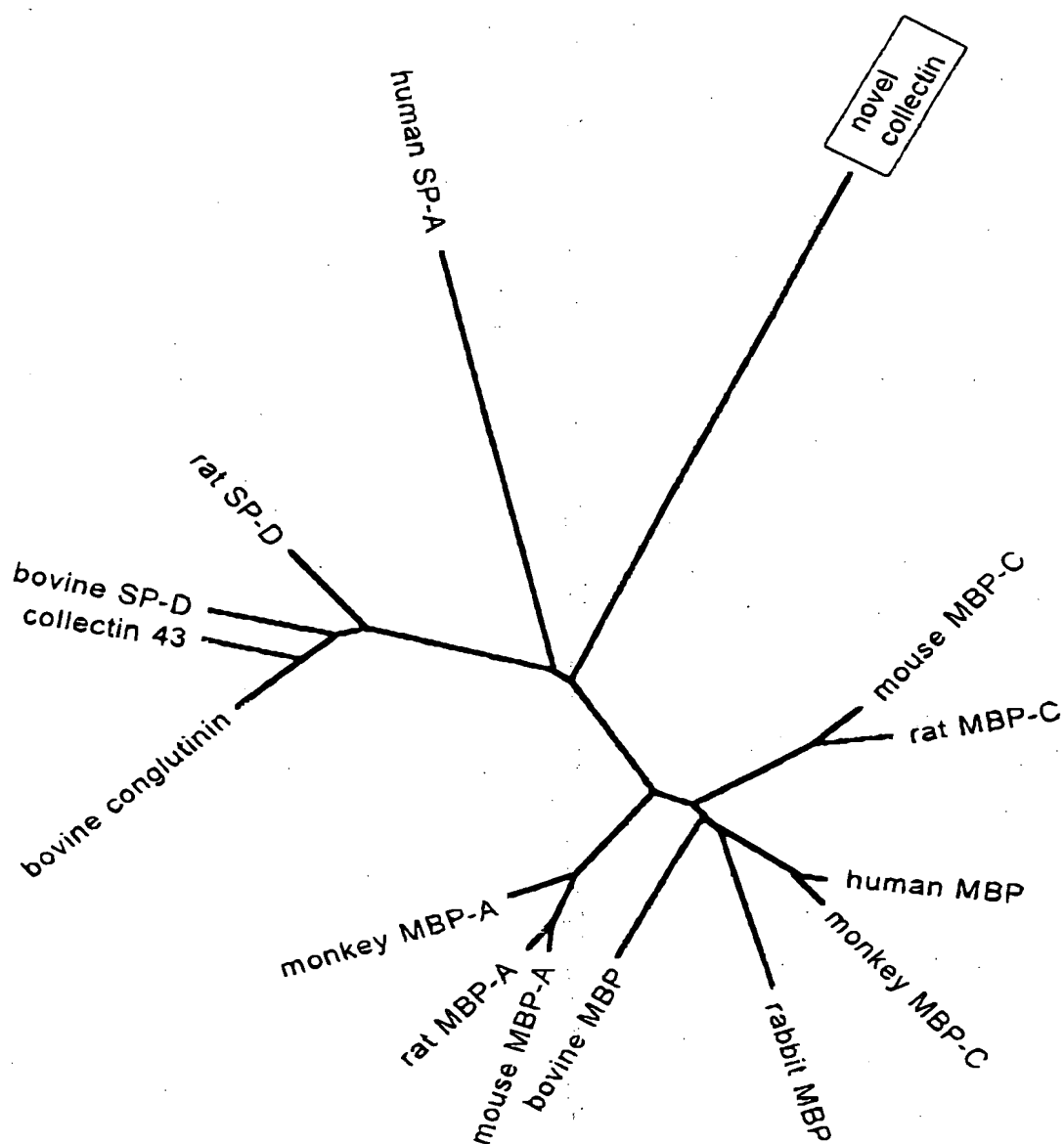


Fig.11